

096429-9141.ST25.txt  
SEQUENCE LISTING

<110> Welch, Rodney A.  
Lathem, Wyndham W.  
Grys, Thomas E.

<120> E. COLI O157:H7 C1-INH-BINDING PROTEIN AND METHODS OF USE

<130> 096429-9141

<140> New Patent Application

<141> 2004-02-25

<150> 10/002,309

<151> 2001-10-26

<150> 60/243,675

<151> 2000-10-26

<160> 25

<170> PatentIn version 3.1

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<212> DNA

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<223> Description of Unknown Organism: E. coli O157:H7 plasmid p0157

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<222> (138)..(2798)

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## 096429-9141.ST25.txt

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Val Pro Glu Gly Gly Ile Asp Phe Thr Pro His Asn Gly Thr Lys Lys
                125          130          135
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## 096429-9141.ST25.txt

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 Ala Glu Val Asn Lys Leu Ser Asp Ala Ser Gly Ser Ser Ile His Ser  
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 Ser His Glu Val Gly His Asn Tyr Gly Leu Gly His Tyr Val Asp Gly  
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&lt;223&gt; Description of Unknown Organism: E. coli O157:H7 plasmid pO157

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&lt;213&gt; Synthetic oligonucleotide

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25

&lt;210&gt; 13

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&lt;222&gt; (138)..(2795)

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Ser Leu Ala Ala Glu Val Lys Phe Ala Gln Ser Gln Ile Leu Pro Ala  
45 50 55cat cct aaa gaa ggg gat agt caa cca cat ctg acc agc ctg cgg aaa 362  
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atc Ile 140	att Ile	aat Asn	acg Thr	gtg Val	gct Ala 145	gaa Glu	gta Val	aac Asn	aaa Lys	ctc Leu 150	agt Ser	gat Asp	gcc Ala	agc Ser	ggg Gly 155	602
agt Ser	tct Ser	att Ile	cat His	agc Ser 160	cat His	cta Leu	aca Thr	aat Asn	aat Asn 165	gca Ala	ctg Leu	gtg Val	gag Glu	atc Ile 170	cat His	650
act Thr	gca Ala	aat Asn	ggg Gly 175	cgt Arg	tgg Trp	gta Val	aga Arg	gac Asp 180	att Ile	tat Tyr	ctg Leu	ccg Pro	cag Gln 185	gga Gly	ccc Pro	698
gac Asp	ctt Leu	gaa Glu 190	ggg Gly	aag Lys	atg Met	gtt Val	cgc Arg 195	ttt Phe	gtt Val	tcg Ser	tct Ser	gca Ala 200	ggc Gly	tat Tyr	agt Ser	746
tca Ser	acg Thr 205	gtt Val	ttt Phe	tat Tyr	ggg Gly	gat Asp 210	cga Arg	aaa Lys	gtc Val	aca Thr	ctc Leu 215	tcg Ser	gtg Val	ggg Gly	aac Asn	794
act Thr 220	ctt Leu	ctg Leu	ttc Phe	aaa Lys	tat Tyr 225	gta Val	aat Asn	ggg Gly	cag Gln	tgg Trp 230	ttc Phe	cgc Arg	tcc Ser	ggg Gly	gaa Glu 235	842
ctg Leu	gag Glu	aat Asn	aat Asn	cga Arg 240	atc Ile	act Thr	tat Tyr	gct Ala	cag Gln 245	cat His	att Ile	tgg Trp	agt Ser	gct Ala 250	gaa Glu	890
ctg Leu	cct Pro	gcg Ala	cac His 255	tgg Trp	atc Ile	gtg Val	cct Pro	ggg Gly 260	tta Leu	aac Asn	ttg Leu	gtg Val	att Ile 265	aaa Lys	cag Gln	938
ggc Gly	aat Asn 270	ctg Leu	agc Ser	ggg Gly	cgc Arg	cta Leu	aat Asn 275	gat Asp	atc Ile	aag Lys	att Ile	gga Gly 280	gca Ala	ccg Pro	ggg Gly	986
gag Glu 285	ctg Leu	ttg Leu	ttg Leu	cat His	aca Thr	att Ile 290	gat Asp	atc Ile	ggg Gly	atg Met	ttg Leu 295	acc Thr	act Thr	ccc Pro	cgg Arg	1034
gat Asp 300	cgc Arg	ttt Phe	gat Asp	ttt Phe	gcc Ala 305	aaa Lys	gac Asp	aaa Lys	gaa Glu	gca Ala 310	cat His	agg Arg	gaa Glu	tat Tyr	ttc Phe 315	1082
cag Gln	acc Thr	att Ile	cct Pro	gta Val 320	agt Ser	cgt Arg	atg Met	att Ile	gtt Val 325	aat Asn	aat Asn	tat Tyr	gcg Ala	cct Pro 330	cta Leu	1130
cac His	cta Leu	aag Lys	gaa Glu 335	gtt Val	atg Met	tta Leu	cca Pro	acc Thr 340	gga Gly	gag Glu	tta Leu	ttg Leu	aca Thr 345	gat Asp	atg Met	1178
gat Asp	cca Pro	gga Gly 350	aat Asn	ggg Gly	ggg Gly	tgg Trp	cat His 355	agt Ser	ggg Gly	aca Thr	atg Met	cgt Arg 360	caa Gln	aga Arg	ata Ile	1226
ggg Gly	aaa Lys 365	gaa Glu	ttg Leu	gtt Val	tcg Ser	cat His 370	ggc Gly	att Ile	gat Asp	aat Asn	gct Ala 375	aac Asn	tat Tyr	ggg Gly	tta Leu	1274

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aat Asn 380	agt Ser	acc Thr	gca Ala	ggc Gly	tta Leu 385	ggg Gly	gag Glu	aat Asn	agt Ser	cat His 390	cca Pro	tat Tyr	gta Val	gtt Val	gcg Ala 395	1322
caa Gln	tta Leu	gcg Ala	gca Ala	cat His 400	aat Asn	agc Ser	cgc Arg	ggg Gly	aat Asn 405	tat Tyr	gct Ala	aat Asn	ggc Gly	atc Ile 410	cag Gln	1370
gtt Val	cat His	ggg Gly	ggc Gly 415	tcc Ser	gga Gly	ggg Gly	ggg Gly	gga Gly 420	att Ile	gtt Val	act Thr	tta Leu	gat Asp 425	tcc Ser	aca Thr	1418
ttg Leu	ggg Gly	aat Asn 430	gag Glu	ttc Phe	agt Ser	cat His	gat Asp 435	gtt Val	ggg Gly	cat His	aat Asn	tat Tyr 440	ggg Gly	ctt Leu	ggg Gly	1466
cat His	tat Tyr 445	gta Val	gat Asp	ggg Gly	ttc Phe	aag Lys 450	ggg Gly	tct Ser	gta Val	cat His	cgt Arg 455	agt Ser	gca Ala	gaa Glu	aat Asn	1514
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tgt Cys	caa Gln	gaa Glu	ccg Pro 495	ttt Phe	gat Asp	gga Gly	cac His	aaa Lys 500	ttt Phe	ggg Gly	ttt Phe	gac Asp	gcc Ala 505	atg Met	gcg Ala	1658
gga Gly	ggc Gly	agc Ser 510	cct Pro	ttc Phe	tct Ser	gct Ala	gca Ala 515	aac Asn	cgt Arg	ttc Phe	aca Thr	atg Met 520	tat Tyr	act Thr	ccg Pro	1706
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gat Asp 540	agc Ser	cgt Arg	tcc Ser	tcc Ser	acc Thr 545	ggc Gly	ttc Phe	agc Ser	aag Lys	tgg Trp 550	aat Asn	gca Ala	gat Asp	acg Thr	cag Gln 555	1802
gaa Glu	atg Met	gaa Glu	ccg Pro	tat Tyr 560	gaa Glu	cac His	acc Thr	att Ile	gac Asp 565	cgt Arg	gcg Ala	gag Glu	cag Gln	att Ile 570	acg Thr	1850
gct Ala	tca Ser	gtc Val	aat Asn 575	gag Glu	cta Leu	agt Ser	gaa Glu	agc Ser 580	aaa Lys	atg Met	gct Ala	gag Glu	ctg Leu 585	atg Met	gca Ala	1898
gag Glu	tac Tyr	gct Ala 590	gtc Val	gtc Val	aaa Lys	gtg Val	cat His 595	atg Met	tgg Trp	aac Asn	ggg Gly	aac Asn 600	tgg Trp	aca Thr	aga Arg	1946
aac Asn	atc Ile 605	tat Tyr	atc Ile	cct Pro	aca Thr	gcc Ala 610	tcc Ser	gca Ala	gat Asp	aat Asn	aga Arg 615	ggc Gly	agt Ser	atc Ile	ctg Leu	1994
acc Thr 620	atc Ile	aac Asn	cat His	gag Glu	gcc Ala 625	ggg Gly	tat Tyr	aat Asn	agt Ser	tat Tyr 630	ctg Leu	ttt Phe	ata Ile	aat Asn	ggg Gly 635	2042
gac Asp	gaa Glu	aag Lys	gtc Val	gtt Val 640	tcc Ser	cag Gln	ggg Gly	tat Tyr	aaa Lys 645	aag Lys	agc Ser	ttt Phe	gtt Val	tcc Ser 650	gat Asp	2090

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gat Asp	ccg Pro 685	gaa Glu	ggc Gly	acg Thr	ctg Leu	tca Ser 690	agc Ser	tac Tyr	atc Ile	tat Tyr	cct Pro 695	gcg Ala	atg Met	tat Tyr	ggt Gly	2234
gcc Ala 700	tat Tyr	ggc Gly	ttc Phe	act Thr	tat Tyr 705	tcc Ser	gat Asp	gat Asp	agt Ser	cag Gln 710	aat Asn	cta Leu	tcc Ser	gat Asp	aac Asn 715	2282
gac Asp	tgc Cys	cag Gln	ctg Leu	cag Gln 720	gtg Val	gat Asp	acg Thr	aaa Lys	gaa Glu 725	ggg Gly	cag Gln	ttg Leu	cga Arg	ttc Phe 730	aga Arg	2330
ctg Leu	gct Ala	aat Asn	cac His 735	cgg Arg	gct Ala	aac Asn	aac Asn	act Thr 740	gta Val	atg Met	aat Asn	aag Lys	ttc Phe 745	cat His	att Ile	2378
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acc Thr 780	tat Tyr	act Thr	gta Val	aat Asn	ggg Gly 785	cag Gln	gca Ala	ctt Leu	cca Pro	gca Ala 790	aaa Lys	gaa Glu	aac Asn	gag Glu	gga Gly 795	2522
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caa Gln	cgg Arg	tca Ser	gga Gly 815	tat Tyr	agc Ser	ctt Leu	cct Pro	gac Asp 820	tgg Trp	att Ile	gtt Val	ggg Gly	cag Gln 825	gaa Glu	gtc Val	2618
tat Tyr	gtc Val	gac Asp 830	agc Ser	ggg Gly	gct Ala	aaa Lys	gcg Ala 835	aaa Lys	gtg Val	ctg Leu	ctt Leu	tct Ser 840	gac Asp	tgg Trp	gat Asp	2666
aac Asn	ctg Leu 845	tcc Ser	tat Tyr	aac Asn	agg Arg	att Ile 850	ggt Gly	gag Glu	ttt Phe	gta Val	ggt Gly 855	aat Asn	gtg Val	aac Asn	cca Pro	2714
gct Ala 860	gat Asp	atg Met	aaa Lys	aaa Lys	gtt Val 865	aaa Lys	gcc Ala	tgg Trp	aac Asn	gga Gly 870	cag Gln	tat Tyr	ttg Leu	gac Asp	ttc Phe 875	2762
agt Ser	aaa Lys	cct Pro	agg Arg	tca Ser 880	atg Met	agg Arg	gtt Val	gta Val	tat Tyr 885	aaa Lys						2795

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&lt;211&gt; 886

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&lt;220&gt;

&lt;223&gt; Description of Unknown Organism: E. coli O157:H7 plasmid p0157

&lt;400&gt; 19

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Gly Val Phe Ser Ala Thr Ala Ala Asp Asn Asn Ser Ala Ile Tyr Phe  
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Asn Thr Ser Gln Pro Ile Asn Asp Leu Gln Gly Ser Leu Ala Ala Glu  
 35 40 45

Val Lys Phe Ala Gln Ser Gln Ile Leu Pro Ala His Pro Lys Glu Gly  
 50 55 60

Asp Ser Gln Pro His Leu Thr Ser Leu Arg Lys Ser Leu Leu Leu Val  
 65 70 75 80

Arg Pro Val Lys Ala Asp Asp Lys Thr Pro Val Gln Val Glu Ala Arg  
 85 90 95

Asp Asp Asn Asn Lys Ile Leu Gly Thr Leu Thr Leu Tyr Pro Pro Ser  
 100 105 110

Ser Leu Pro Asp Thr Ile Tyr His Leu Asp Gly Val Pro Glu Gly Gly  
 115 120 125

Ile Asp Phe Thr Pro His Asn Gly Thr Lys Lys Ile Ile Asn Thr Val  
 130 135 140

Ala Glu Val Asn Lys Leu Ser Asp Ala Ser Gly Ser Ser Ile His Ser  
 145 150 155 160

His Leu Thr Asn Asn Ala Leu Val Glu Ile His Thr Ala Asn Gly Arg  
 165 170 175

Trp Val Arg Asp Ile Tyr Leu Pro Gln Gly Pro Asp Leu Glu Gly Lys  
 180 185 190

Met Val Arg Phe Val Ser Ser Ala Gly Tyr Ser Ser Thr Val Phe Tyr  
 195 200 205

Gly Asp Arg Lys Val Thr Leu Ser Val Gly Asn Thr Leu Leu Phe Lys  
 210 215 220

Tyr Val Asn Gly Gln Trp Phe Arg Ser Gly Glu Leu Glu Asn Asn Arg  
 225 230 235 240



Ile Thr Tyr Ala Gln His Ile Trp Ser Ala Glu Leu Pro Ala His Trp  
 245 250 255  
 Ile Val Pro Gly Leu Asn Leu Val Ile Lys Gln Gly Asn Leu Ser Gly  
 260 265 270  
 Arg Leu Asn Asp Ile Lys Ile Gly Ala Pro Gly Glu Leu Leu Leu His  
 275 280 285  
 Thr Ile Asp Ile Gly Met Leu Thr Thr Pro Arg Asp Arg Phe Asp Phe  
 290 295 300  
 Ala Lys Asp Lys Glu Ala His Arg Glu Tyr Phe Gln Thr Ile Pro Val  
 305 310 315 320  
 Ser Arg Met Ile Val Asn Asn Tyr Ala Pro Leu His Leu Lys Glu Val  
 325 330 335  
 Met Leu Pro Thr Gly Glu Leu Leu Thr Asp Met Asp Pro Gly Asn Gly  
 340 345 350  
 Gly Trp His Ser Gly Thr Met Arg Gln Arg Ile Gly Lys Glu Leu Val  
 355 360 365  
 Ser His Gly Ile Asp Asn Ala Asn Tyr Gly Leu Asn Ser Thr Ala Gly  
 370 375 380  
 Leu Gly Glu Asn Ser His Pro Tyr Val Val Ala Gln Leu Ala Ala His  
 385 390 395 400  
 Asn Ser Arg Gly Asn Tyr Ala Asn Gly Ile Gln Val His Gly Gly Ser  
 405 410 415  
 Gly Gly Gly Gly Ile Val Thr Leu Asp Ser Thr Leu Gly Asn Glu Phe  
 420 425 430  
 Ser His Asp Val Gly His Asn Tyr Gly Leu Gly His Tyr Val Asp Gly  
 435 440 445  
 Phe Lys Gly Ser Val His Arg Ser Ala Glu Asn Asn Asn Ser Thr Trp  
 450 455 460  
 Gly Trp Asp Gly Asp Lys Lys Arg Phe Ile Pro Asn Phe Tyr Pro Ser  
 465 470 475 480  
 Gln Thr Asn Glu Lys Ser Cys Leu Asn Asn Gln Cys Gln Glu Pro Phe  
 485 490 495  
 Asp Gly His Lys Phe Gly Phe Asp Ala Met Ala Gly Gly Ser Pro Phe  
 500 505 510

Ser Ala Ala Asn Arg Phe Thr Met Tyr Thr Pro Asn Ser Ser Ala Ile  
 515 520 525  
 Ile Gln Arg Phe Phe Glu Asn Lys Ala Val Phe Asp Ser Arg Ser Ser  
 530 535 540  
 Thr Gly Phe Ser Lys Trp Asn Ala Asp Thr Gln Glu Met Glu Pro Tyr  
 545 550 555 560  
 Glu His Thr Ile Asp Arg Ala Glu Gln Ile Thr Ala Ser Val Asn Glu  
 565 570 575  
 Leu Ser Glu Ser Lys Met Ala Glu Leu Met Ala Glu Tyr Ala Val Val  
 580 585 590  
 Lys Val His Met Trp Asn Gly Asn Trp Thr Arg Asn Ile Tyr Ile Pro  
 595 600 605  
 Thr Ala Ser Ala Asp Asn Arg Gly Ser Ile Leu Thr Ile Asn His Glu  
 610 615 620  
 Ala Gly Tyr Asn Ser Tyr Leu Phe Ile Asn Gly Asp Glu Lys Val Val  
 625 630 635 640  
 Ser Gln Gly Tyr Lys Lys Ser Phe Val Ser Asp Gly Gln Phe Trp Lys  
 645 650 655  
 Glu Arg Asp Val Val Asp Thr Arg Glu Ala Arg Lys Pro Glu Gln Phe  
 660 665 670  
 Gly Val Pro Val Thr Thr Leu Val Gly Tyr Tyr Asp Pro Glu Gly Thr  
 675 680 685  
 Leu Ser Ser Tyr Ile Tyr Pro Ala Met Tyr Gly Ala Tyr Gly Phe Thr  
 690 695 700  
 Tyr Ser Asp Asp Ser Gln Asn Leu Ser Asp Asn Asp Cys Gln Leu Gln  
 705 710 715 720  
 Val Asp Thr Lys Glu Gly Gln Leu Arg Phe Arg Leu Ala Asn His Arg  
 725 730 735  
 Ala Asn Asn Thr Val Met Asn Lys Phe His Ile Asn Val Pro Thr Glu  
 740 745 750  
 Ser Gln Pro Thr Gln Ala Thr Leu Val Cys Asn Asn Lys Ile Leu Asp  
 755 760 765  
 Thr Lys Ser Leu Thr Pro Ala Pro Glu Gly Leu Thr Tyr Thr Val Asn  
 770 775 780

Gly Gln Ala Leu Pro Ala Lys Glu Asn Glu Gly Cys Ile Val Ser Val  
785 790 795 800  
Asn Ser Gly Lys Arg Tyr Cys Leu Pro Val Gly Gln Arg Ser Gly Tyr  
805 810 815  
Ser Leu Pro Asp Trp Ile Val Gly Gln Glu Val Tyr Val Asp Ser Gly  
820 825 830  
Ala Lys Ala Lys Val Leu Leu Ser Asp Trp Asp Asn Leu Ser Tyr Asn  
835 840 845  
Arg Ile Gly Glu Phe Val Gly Asn Val Asn Pro Ala Asp Met Lys Lys  
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